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Abstract

## Gut Microbiome Composition Is Associated with Blood Glucose Control and Dietary Intake in People with Type 1 Diabetes †

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Abstract: Background: Blood glucose control remains a challenge for type 1 diabetes (T1D) patients. Previous studies have shown an association between gut microbiota composition and T1D pathogenesis. However, little is known about the composition of the gut microbiota and its association with host blood glucose control and diet in people with T1D. Objective: We explored the relationship of gut microbiome composition with blood glucose control and dietary intake in people with T1D. Research design and methods: In a cross-sectional study, a metagenomic shotgun sequencing analysis of the gut microbiome obtained from fecal samples was performed in 101 individuals with T1D. Dietary intakes were assessed by using the European Prospective Investigation into Cancer and Nutrition (EPIC) questionnaire. Blood glucose control was assessed by continuous glucose monitoring and expressed as time-in-range (TIR), time spent in the blood glucose interval 70-180 mg/dL. Spearman's correlation analysis was used to determine the correlation between gut microbiota composition, blood glucose control, and dietary intake. Results: TIR correlated positively with the abundance of Bacilli (r = 0.258, p = 0.027) and negatively with the Lachnospiraceae family (r = -0.238, p = 0.024), Mediterraneibacter (r = -0.249, p = 0.034), Coprococcus genus (r = -0.286, p = 0.016), Coprococcus comes (r = -0.257, p = 0.028), and Ruminococcus torques (r = -0.261, p = 0.026). The presence of these taxa was associated with the intake of various foods: Bacilli correlated positively with dairy products (r = 0.307, p = 0.002) and negatively with olive oil (r = -0.207, p = 0.041) and meat products (r = -0.255, p = 0.012). Lachnospiraceae correlated negatively with cereals (r = -0.263, p = 0.009). Mediterraneibacter correlated positively with meat and meat products (r = 0.230, p = 0.023). Ruminococcus torques correlated negatively with fruit intake (r = -0.227, p = 0.025). Discussion: Our findings highlight that gut microbiota composition may be related to blood glucose control in T1D and dietary factors may have a role in this interplay. Further investigations are needed to address whether these findings are causally linked and whether to target these gut microbiota taxa.

Keywords: gut microbiome; glycemia; time-in-range; diet



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